

## SEQUENCE LISTING

<110> TALL, ALAN R  
 WELCH, CARRIE L  
 LIANG, CHIEN-PING

<120> ATHEROSCLEROSIS SUSECPTIBILITY GENE LOCUS 1 ( ATHSQ1) AND ATHEROSCLERO  
 SIS  
 SUSCEPTIBILITY GENE LOCUS 2 (ATHSQ2)

<130> 0575/64077

<160> 40

<170> PatentIn version 3.1

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 aag tca tgt ggc aag aag cct aaa gag gag tcc cag aga gaa ctc aag 96  
 Lys Ser Cys Gly Lys Lys Pro Lys Glu Glu Ser Gln Arg Glu Leu Lys  
 20 25 30  
 gga aag ata gac acc atc acc cgg aag ctg gac gag aaa tcc aaa gag 144  
 Gly Lys Ile Asp Thr Ile Thr Arg Lys Leu Asp Glu Lys Ser Lys Glu  
 35 40 45  
 cag gag gag ctt ctg cag atg att cag aac ctc caa gaa gcc ctg cag 192  
 Gln Glu Glu Leu Leu Gln Met Ile Gln Asn Leu Gln Glu Ala Leu Gln  
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 Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln Arg Glu Leu Lys Gly Lys  
 65 70 75 80  
 ata gac acc ctc acc ttg aag ctg aac gag aaa tcc aaa gag cag gag 288  
 Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser Lys Glu Gln Glu  
 85 90 95  
 gag ctt cta cag aag aat cag aac ctc caa gaa gcc ctg caa aga gct 336  
 Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala Leu Gln Arg Ala  
 100 105 110  
 gca aac ttt tca ggt cct tgt cca caa gac tgg ctc tgg cat aaa gaa 384  
 Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu Trp His Lys Glu  
 115 120 125  
 aac tgt tac ctc ttc cat ggg ccc ttt ggc tgg gaa aaa aac cgg cag 432  
 Asn Cys Tyr Leu Phe His Gly Pro Phe Gly Trp Glu Lys Asn Arg Gln  
 130 135 140  
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 145 150 155 160  
 gat ctg aca ttc atc tta caa gca att tcc cat acc acc tcc cca ttc 528  
 Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr Thr Ser Pro Phe  
 165 170 175  
 tgg att gga ttg cat cgg aag aag cct ggc caa cca tgg cta tgg gag 576  
 Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro Trp Leu Trp Glu  
 180 185 190  
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 Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr Arg Gly Val Ser  
 195 200 205  
 tta cag cta tat tca tca agc aac tgt gca tac ctt caa gac gga gct 672  
 Leu Gln Leu Tyr Ser Ser Ser Asn Cys Ala Tyr Leu Gln Asp Gly Ala  
 210 215 220  
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 Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser Ile Cys Gln Lys  
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744

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 35 40 45

Gln Glu Glu Leu Leu Gln Met Ile Gln Asn Leu Gln Glu Ala Leu Gln  
 50 55 60

Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln Arg Glu Leu Lys Gly Lys  
 65 70 75 80

Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser Lys Glu Gln Glu  
 85 90 95

Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala Leu Gln Arg Ala  
 100 105 110

Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu Trp His Lys Glu  
 115 120 125

Asn Cys Tyr Leu Phe His Gly Pro Phe Gly Trp Glu Lys Asn Arg Gln  
 130 135 140

Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile Asn Gly Ala Asp  
 145 150 155 160

Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr Thr Ser Pro Phe  
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Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro Trp Leu Trp Glu  
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Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr Arg Gly Val Ser  
195 200 205

Leu Gln Leu Tyr Ser Ser Ser Asn Cys Ala Tyr Leu Gln Asp Gly Ala  
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Lys Ser Cys Gly Lys Lys Pro Lys Glu Glu Ser Gln Arg Glu Leu Lys  
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gga aag ata gac acc ctc acc ttg aag ctg aac gag aaa tcc aaa gag 144  
Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser Lys Glu  
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cag gag gag ctt cta cag aag aat cag aac ctc caa gaa gcc ctg caa 192  
Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala Leu Gln  
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Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu Trp His  
65 70 75 80  
aaa gaa aac tgt tac ctc ttc cat ggg ccc ttt agc tgg gaa aaa aac 288  
Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu Lys Asn  
85 90 95  
cgg cag acc tgc caa tct ttg ggt ggc cag tta cta caa att aat ggt 336  
Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile Asn Gly  
100 105 110  
gca gat gat ctg aca ttc atc tta caa gca att tcc cat acc acc tcc 384

Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr Thr Ser  
115 120 125

cca ttc tgg att gga ttg cat cgg aag aag cct ggc caa cca tgg cta 432  
Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro Trp Leu  
130 135 140

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Trp Glu Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr Arg Gly  
145 150 155 160

gtt tct tta cag cta tat tca tca ggc aac tgt gca tac ctt caa gac 528  
Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu Gln Asp  
165 170 175

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Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser Ile Cys  
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35 40 45

Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala Leu Gln  
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Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu Trp His  
65 70 75 80

Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu Lys Asn  
85 90 95

Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile Asn Gly  
100 105 110



Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr Thr Ser  
115 120 125

Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro Trp Leu  
130 135 140

Trp Glu Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr Arg Gly  
145 150 155 160

Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu Gln Asp  
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Lys Ser Cys Gly Lys Lys Pro Lys Gly Pro Cys Pro Gln Asp Trp Leu  
20 25 30  
tgg cat aaa gaa aac tgt tac ctc ttc cat ggg ccc ttt agc tgg gaa 144  
Trp His Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu  
35 40 45  
aaa aac cgg cag acc tgc caa tct ttg ggt ggc cag tta cta caa att 192  
Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile  
50 55 60  
aat ggt gca gat gat ctg aca ttc atc tta caa gca att tcc cat acc 240  
Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr  
65 70 75 80  
acc tcc cca ttc tgg att gga ttg cat cgg aag aag cct ggc caa cca 238  
Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro

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Arg Gly Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu				
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caa gac gga gct gtg ttc gct gaa aac tgc att cta att gca ttc agc				432
Gln Asp Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser				
	130	135	140	
ata tgt cag aag aag aca aat cat ttg caa att tag				468
Ile Cys Gln Lys Lys Thr Asn His Leu Gln Ile				
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20 25 30	

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35 40 45	

Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile	
50 55 60	

Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr	
65 70 75 80	

Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro	
85 90 95	

Trp Leu Trp Glu Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr	
100 105 110	

Arg Gly Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu	
115 120 125	

Gln Asp Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser	
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 aag tca tgt ggc aag aag cct aaa ggt ctg cat ttg ctt tct tcc cca 96  
 Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro  
 20 25 30  
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 Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu  
 35 40 45  
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 Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp  
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 65 70 75 80  
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 Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Gln Glu  
 85 90 95  
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 Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu  
 100 105 110  
 aac gag aaa tcc aaa gag cag gag gag ctt cta cag aag aat cag aac 384  
 Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn  
 115 120 125  
 ctc caa gaa gcc ctg caa aga gct gca aac tct tca gag gag tcc cag 432  
 Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln  
 130 135 140  
 aga gaa ctc aag gga aag ata gac acc atc acc cgg aag ctg gac gag 480  
 Arg Glu Leu Lys Gly Lys Ile Asp Thr Ile Thr Arg Lys Leu Asp Glu  
 145 150 155 160

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gaa gcc ctg cag aga gct gca aac tct tca gag gag tcc cag aga gaa      576
Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln Arg Glu
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ctc aag gga aag ata gac acc ctc acc ttg aag ctg aac gag aaa tcc      624
Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser
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                               210                               215                               220

ctg caa aga gct gca aac ttt tca ggt cct tgt cca caa gac tgg ctc      720
Leu Gln Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu
                               225                               230                               235                               240

tgg cat aaa gaa aac tgt tac ctc ttc cat ggg ccc ttt agc tgg gaa      768
Trp His Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu
                               245                               250                               255

aaa aac cgg cag acc tgc caa tct ttg ggt ggc cag tta cta caa att      816
Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile
                               260                               265                               270

aat ggt gca gat gat ctg aca ttc atc tta caa gca att tcc cat acc      864
Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr
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acc tcc cca ttc tgg att gga ttg cat cgg aag aag cct ggc caa cca      912
Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro
                               290                               295                               300

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agg ggc gtt tct tta cag cta tat tca tca ggc aac tgt gca tac ctt      1008
Arg Gly Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu
                               325                               330                               335

caa gac gga gct gtg ttc gct gaa aac tgc att cta att gca ttc agc      1056
Gln Asp Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser
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ata tgt cag aag aag aca aat cat ttg caa att tag      1092
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Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro  
 20 25 30

Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu  
 35 40 45

Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp  
 50 55 60

Leu Leu Lys Gln Tyr Gln Ala Asn Leu Thr Gln Gln Asp Arg Ile Leu  
 65 70 75 80

Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Gln Glu  
 85 90 95

Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu  
 100 105 110

Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn  
 115 120 125

Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln  
 130 135 140

Arg Glu Leu Lys Gly Lys Ile Asp Thr Ile Thr Arg Lys Leu Asp Glu  
 145 150 155 160

Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Met Ile Gln Asn Leu Gln  
 165 170 175

Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln Arg Glu  
 180 185 190

Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser  
 195 200 205

Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala  
 210 215 220

Leu Gln Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu  
 225 230 235 240

Trp His Lys Glu Asn Cys Tyr Leu Phe His Gly Pro Phe Ser Trp Glu

245                      250                      255  
 Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile  
                     260                      265                      270  
 Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr  
                     275                      280                      285  
 Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro  
                     290                      295                      300  
 Trp Leu Trp Glu Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr  
 305                      310                      315                      320  
 Arg Gly Val Ser Leu Gln Leu Tyr Ser Ser Gly Asn Cys Ala Tyr Leu  
                     325                      330                      335  
 Gln Asp Gly Ala Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser  
                     340                      345                      350  
 Ile Cys Gln Lys Lys Thr Asn His Leu Gln Ile  
                     355                      360

<210> 21  
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 <212> DNA  
 <213> Murinae gen. sp.

<220>  
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 <222> (1)..(174)  
 <223>

<220>  
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 <223> Isoform 2

<400> 21  
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 Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln  
 1                      5                      10                      15  
 aag tca tgt ggc aag aag cct aaa ggt ctg cat ttg ctt tct tcc cca                      96  
 Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro  
                     20                      25                      30  
 tgg tgg ttc cct gct gct atg act ctg gtc atc ctc tgc ctg gtg ttg                      144  
 Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu  
                     35                      40                      45  
 tca gtg acc ctt att gta cag tgg aca caa tgatcgtatc ctggaagggc                      194  
 Ser Val Thr Leu Ile Val Gln Trp Thr Gln  
                     50                      55

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agatgttagc ccagcagaag gcagaaaaca cttcacagga atcaaagaag gaactgaaag      254
gaaagataga caccctcacc cagaagctga acgagaaatc caaagagcag gaggagcttc      314
tacagaagaa tcagaacctc caagaagccc tgcaaagagc tgcaaactct tcagaggagt      374
cccagagaga actcaagggg aagatagaca ccataccccc gaagctggac gagaaatcca      434
aagagcagga ggagcttctg cagatgattc agaacctcca agaagccctg cagagagctg      494
caaactcttc agaggagtcc cagagagaac tcaagggaaa gatagacacc ctcaccttga      554
agctgaacga gaaatccaaa gagcaggagg agcttctaca gaagaatcag aacctccaag      614
aagccctgca aagagctgca aactttttcag gtccttgtcc acaagactgg ctctggcata      674
aagaaaactg ttacctcttc cgtggggccct ttactgggaa aaaagccggc agacctgcc      734
atctttgggt ggcagttact acaaattaat gggcagatg      773

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<210> 22
<211> 58
<212> PRT
<213> Murinae gen. sp.

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<220>
<221> misc_feature
<223> Isoform 2

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<400> 22

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Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
1          5          10          15

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Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro
          20          25          30

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```

Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu
          35          40          45

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Ser Val Thr Leu Ile Val Gln Trp Thr Gln
          50          55

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<210> 23
<211> 495
<212> DNA
<213> Murinae gen. sp.

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<220>
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<222> (1)..(495)
<223>

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<220>
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<223> Isoform 3

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<400> 23  
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 Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln  
 1 5 10 15  
  
 aag tca tgt ggc aag aag cct aaa ggt ctg cat ttg ctt tct tcc cca 96  
 Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro  
 20 25 30  
  
 tgg tgg ttc cct gct gct atg act ctg gtc atc ctc tgc ctg gtg ttg 144  
 Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu  
 35 40 45  
  
 tca gtg acc ctt att gta cag tgg aca caa tta cgc cag gta tct gac 192  
 Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp  
 50 55 60  
  
 ctc tta aaa caa tac caa gcg aac ctt act cag cag gat cgt atc ctg 240  
 Leu Leu Lys Gln Tyr Gln Ala Asn Leu Thr Gln Gln Asp Arg Ile Leu  
 65 70 75 80  
  
 gaa ggg cag atg tta gcc cag cag aag gca gaa aac act tca ccg caa 288  
 Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Pro Gln  
 85 90 95  
  
 tca aag aag gaa ctg aaa gga aag ata gac acc ctc acc cag aag ctg 336  
 Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu  
 100 105 110  
  
 aac gag aaa tcc aaa gag cag gag gag ctt cta cag aag aat cag aac 384  
 Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn  
 115 120 125  
  
 ctc caa gaa gcc ctg caa aga gct gca aac tct tca gag gag tcc cag 432  
 Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln  
 130 135 140  
  
 aga gaa ctc aag gga aag ata gac acc ctc acc ttg aag ctg aac gag 480  
 Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu  
 145 150 155 160  
  
 aaa tcc aaa gag cag 495  
 Lys Ser Lys Glu Gln  
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<210> 24  
 <211> 165  
 <212> PRT  
 <213> Murinae gen. sp.

<220>  
 <221> misc\_feature  
 <223> Isoform 3

<400> 24

Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln  
 1 5 10 15



Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro  
                   20                  25                  30  
 Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu  
           35                  40                  45  
 Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp  
           50                  55                  60  
 Leu Leu Lys Gln Tyr Gln Ala Asn Leu Thr Gln Gln Asp Arg Ile Leu  
   65                  70                  75                  80  
 Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Pro Gln  
                   85                  90                  95  
 Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu  
                   100                  105                  110  
 Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn  
           115                  120                  125  
 Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln  
   130                  135                  140  
 Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu  
   145                  150                  155                  160  
 Lys Ser Lys Glu Gln  
                   165

<210> 25  
 <211> 621  
 <212> DNA  
 <213> Murinae gen. sp.

<220>  
 <221> CDS  
 <222> (1)..(621)  
 <223>

<220>  
 <221> misc\_feature  
 <223> Isoform 4

<400> 25  
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 Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln  
 1                  5                  10                  15  
 aag tca tgt ggc aag aag cct aaa ggt ctg cat ttg ctt tct tcc cca 96  
 Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro

20										25					30					
tgg	tgg	ttc	cct	gct	gct	atg	act	ctg	gtc	atc	ctc	tgc	ctg	gtg	ttg	144				
Trp	Trp	Phe	Pro	Ala	Ala	Met	Thr	Leu	Val	Ile	Leu	Cys	Leu	Val	Leu					
		35					40					45								
tca	gtg	acc	ctt	att	gta	cag	tgg	aca	caa	tta	cgc	cag	gta	tct	gac	192				
Ser	Val	Thr	Leu	Ile	Val	Gln	Trp	Thr	Gln	Leu	Arg	Gln	Val	Ser	Asp					
	50					55					60									
ctc	tta	aaa	caa	tac	caa	gcg	aac	ctt	act	cag	cag	gat	cgt	atc	ctg	240				
Leu	Leu	Lys	Gln	Tyr	Gln	Ala	Asn	Leu	Thr	Gln	Gln	Asp	Arg	Ile	Leu					
65					70					75					80					
gaa	ggg	cag	atg	tta	gcc	cag	cag	aag	gca	gaa	aac	act	tca	cag	gaa	288				
Glu	Gly	Gln	Met	Leu	Ala	Gln	Gln	Lys	Ala	Glu	Asn	Thr	Ser	Gln	Glu					
			85						90					95						
tca	aag	aag	gaa	ctg	aaa	gga	aag	ata	gac	acc	ctc	acc	cag	aag	ctg	336				
Ser	Lys	Lys	Glu	Leu	Lys	Gly	Lys	Ile	Asp	Thr	Leu	Thr	Gln	Lys	Leu					
			100					105					110							
aac	gag	aaa	tcc	aaa	gag	cag	gag	gag	ctt	cta	cag	aag	aat	cag	aac	384				
Asn	Glu	Lys	Ser	Lys	Glu	Gln	Glu	Glu	Leu	Leu	Gln	Lys	Asn	Gln	Asn					
		115					120					125								
ctc	caa	gaa	gcc	ctg	caa	aga	gct	gca	aac	ttt	tca	ggg	cct	tgt	cca	432				
Leu	Gln	Glu	Ala	Leu	Gln	Arg	Ala	Ala	Asn	Phe	Ser	Gly	Pro	Cys	Pro					
	130					135					140									
caa	gac	tgg	ctc	tgg	cat	aaa	gaa	aac	tgt	tac	ctc	ttc	cat	ggg	ccc	480				
Gln	Asp	Trp	Leu	Trp	His	Lys	Glu	Asn	Cys	Tyr	Leu	Phe	His	Gly	Pro					
145					150					155					160					
ttt	agc	tgg	gaa	aaa	aac	cgg	cag	acc	tgc	caa	tct	ttg	ggg	ggc	cag	528				
Phe	Ser	Trp	Glu	Lys	Asn	Arg	Gln	Thr	Cys	Gln	Ser	Leu	Gly	Gly	Gln					
				165					170					175						
tta	cta	caa	att	aat	ggg	gca	gat	gat	ctg	aca	ttc	atc	tta	caa	gca	576				
Leu	Leu	Gln	Ile	Asn	Gly	Ala	Asp	Asp	Leu	Thr	Phe	Ile	Leu	Gln	Ala					
			180					185					190							
att	tcc	cat	acc	acc	tcc	ccg	ttc	tgg	att	gga	ttg	cat	cgg	aag		621				
Ile	Ser	His	Thr	Thr	Ser	Pro	Phe	Trp	Ile	Gly	Leu	His	Arg	Lys						
		195					200					205								

<210> 26  
 <211> 207  
 <212> PRT  
 <213> Murinae gen. sp.

<220>  
 <221> misc\_feature  
 <223> Isoform 4

<400> 26

Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln  
 1 5 10 15

Lys Ser Cys Gly Lys Lys Pro Lys Gly Leu His Leu Leu Ser Ser Pro

20

25

30

Trp Trp Phe Pro Ala Ala Met Thr Leu Val Ile Leu Cys Leu Val Leu  
35 40 45

Ser Val Thr Leu Ile Val Gln Trp Thr Gln Leu Arg Gln Val Ser Asp  
50 55 60

Leu Leu Lys Gln Tyr Gln Ala Asn Leu Thr Gln Gln Asp Arg Ile Leu  
65 70 75 80

Glu Gly Gln Met Leu Ala Gln Gln Lys Ala Glu Asn Thr Ser Gln Glu  
85 90 95

Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys Leu  
100 105 110

Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln Asn  
115 120 125

Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly Pro Cys Pro  
130 135 140

Gln Asp Trp Leu Trp His Lys Glu Asn Cys Tyr Leu Phe His Gly Pro  
145 150 155 160

Phe Ser Trp Glu Lys Asn Arg Gln Thr Cys Gln Ser Leu Gly Gly Gln  
165 170 175

Leu Leu Gln Ile Asn Gly Ala Asp Asp Leu Thr Phe Ile Leu Gln Ala  
180 185 190

Ile Ser His Thr Thr Ser Pro Phe Trp Ile Gly Leu His Arg Lys  
195 200 205

<210> 27

<211> 712

<212> DNA

<213> Murinae gen. sp.

<220>

<221> misc\_feature

<223> Isoform 5

<400> 27

atgacttttg atgacaagat gaagcctgcg aatgacgagc ctgatgagaa gtcattgtggc 60

aagaagccta aaggctctgca tttgctttct tccccatggg ggttccctgc tgctatgact 120

ctggatcatcc tctgcctggg gttgtcagtg acccttattg tacagtggac acaatgatcg 180

tatcctggaa gggcagatgt tagcccagca gaaggcagaa aacacttcac aggaatcaaa 240  
gaaggaactg aaaggaaaga tagacaccct caccagaag ctgaacgact ccaaagagca 300  
ggaggagcta ccccccccc gaacctccaa gaagccctgc aaagagctgc aaactcttca 360  
ggtccttgtc cacaagactg gctctggcat aaagaaaact gttacctctt ccatgggccc 420  
tttagctggg aaaaaaaccg gcagacctgc caatctttgg gtgggcagtt actacaaatt 480  
aatggtgcag atgatctgac attcatctta caagcaattt cccataccac ctccccctct 540  
tggattggat tgcacgga gaagcctggc aaccatgggt atgggagaat ggaacttctt 600  
gaattttaat ttttaagaca ggcgttttt acagtttttc ataaggactt gtgatactta 660  
gagggctggg ttcgttgaaa tgattctatt ggtagcatg tagaaaaaa tt 712

<210> 28  
<211> 721  
<212> DNA  
<213> Murinae gen. sp.

<220>  
<221> misc\_feature  
<223> Isoform 6

<400> 28  
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aagaagccta aaggtctgca tttgctttct tccccatggg gggtccctgc tgctatgact 120  
ctggtcatcc tctgcctggt gttgtcagtg acccttattg tacagtggac acaataggag 180  
tcccagagag aactcaaggg aaagatagac accctcacct tgaagctgaa cgagaaatcc 240  
aaagagcagg aggagcttct acagaagaat cagaacctcc aagaagccct gcaaagagct 300  
gcaaactttt caggtccttg tccacaagac tggctctggc ataaagaaaa ctgttacctc 360  
ttccatgggc ctttagctg ggaaaaaac cggcagacct gccaatcttt ggggtggccg 420  
ttactacaaa ttaatggtgc agatgatctg acattcatct tacaagcaat tccccatacc 480  
acctccccgt tctggattgg attgcatcgg aagaagcctg gccaacctat gctatgggag 540  
aatggaactc ctttgaattt tcaattcttt aagaccaggg gcgtttcttt acagctatat 600  
tcatcaggca actgtgcata ctttcaagac ggactgtgtt cgctgaaaac tgcattctaa 660  
ttgcattcag catatgtcaa aagaagacaa atcatttgca aatttagtga atctaaagaa 720  
t 721

<210> 29  
<211> 46  
<212> PRT  
<213> Murinae gen. sp.

<220>  
 <221> MISC\_FEATURE  
 <223> ISOFORM 1 REPEAT #1

<400> 29

Glu Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys  
 1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln  
 20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu  
 35 40 45

<210> 30  
 <211> 46  
 <212> PRT  
 <213> Murinae gen. sp.

<220>  
 <221> MISC\_FEATURE  
 <223> ISOFORM 1 REPEAT #2

<400> 30

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Ile Thr Arg Lys  
 1 5 10 15

Leu Asp Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Met Ile Gln  
 20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu  
 35 40 45

<210> 31  
 <211> 46  
 <212> PRT  
 <213> Murinae gen. sp.

<220>  
 <221> MISC\_FEATURE  
 <223> ISOFORM 1 REPEAT #3

<400> 31

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys  
 1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln  
 20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly  
           35                          40                          45

<210> 32  
 <211> 46  
 <212> PRT  
 <213> Murinae gen. sp.

<220>  
 <221> MISC\_FEATURE  
 <223> ISOFORM 3 REPEAT #1

<400> 32

Gln Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys  
   1                          5                          10                          15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln  
           20                          25                          30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu  
           35                          40                          45

<210> 33  
 <211> 24  
 <212> PRT  
 <213> Murinae gen. sp.

<220>  
 <221> MISC\_FEATURE  
 <223> ISOFORM 3 REPEAT #3 PARTIAL

<400> 33

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys  
   1                          5                          10                          15

Leu Asn Glu Lys Ser Lys Glu Gln  
           20

<210> 34  
 <211> 46  
 <212> PRT  
 <213> Murinae gen. sp.

<220>  
 <221> MISC\_FEATURE  
 <223> ISOFORM 4 REPEAT #1

<400> 34

Glu Ser Lys Lys Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Gln Lys  
   1                          5                          10                          15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln  
 20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly  
 35 40 45

<210> 35  
 <211> 46  
 <212> PRT  
 <213> Murinae gen. sp.  
 <220>  
 <221> MISC\_FEATURE  
 <223> ISOFORM 7 REPEAT#2

<400> 35

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Ile Thr Arg Lys  
 1 5 10 15

Leu Asp Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Met Ile Gln  
 20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Ser Ser Glu  
 35 40 45

<210> 36  
 <211> 46  
 <212> PRT  
 <213> Murinae gen. sp.  
 <220>  
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 <223> ISOFORM 7 REPEAT#3

<400> 36

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys  
 1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln  
 20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly  
 35 40 45

<210> 37  
 <211> 46  
 <212> PRT  
 <213> Murinae gen. sp.  
 <220>

<221> MISC\_FEATURE  
 <223> ISOFORM 8 REPEAT#3

<400> 37

Glu Ser Gln Arg Glu Leu Lys Gly Lys Ile Asp Thr Leu Thr Leu Lys  
 1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Glu Glu Leu Leu Gln Lys Asn Gln  
 20 25 30

Asn Leu Gln Glu Ala Leu Gln Arg Ala Ala Asn Phe Ser Gly  
 35 40 45

<210> 38  
 <211> 46  
 <212> PRT  
 <213> Homo sapiens

<400> 38

Glu Ser Glu Asn Glu Leu Lys Glu Met Ile Glu Thr Leu Ala Arg Lys  
 1 5 10 15

Leu Asn Glu Lys Ser Lys Glu Gln Met Glu Leu His His Gln Asn Leu  
 20 25 30

Asn Leu Gln Glu Thr Leu Lys Arg Val Ala Asn Cys Ser Ala  
 35 40 45

<210> 39  
 <211> 44  
 <212> PRT  
 <213> Unknown

<220>  
 <223> SIGNATURE SEQUENCE

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(43)  
 <223> X = ANY AMINO ACID

<400> 39

Ser Xaa Xaa Glu Leu Lys Xaa Xaa Ile Xaa Thr Xaa Xaa Xaa Lys Leu  
 1 5 10 15

Xaa Glu Lys Ser Lys Glu Gln Xaa Glu Leu Xaa Xaa Xaa Xaa Xaa Asn  
 20 25 30

Leu Gln Glu Xaa Leu Xaa Arg Xaa Ala Asn Xaa Ser  
 35 40



<210> 40  
 <211> 44  
 <212> PRT  
 <213> Unknown

<220>  
 <223> SIGNATURE SEQUENCE COMMON TO MOUSE AND HUMAN

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(2)  
 <223> X<sub>1</sub> = E, Q, OR K

<220>  
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 <222> (3)..(3)  
 <223> X = N, R, OR K

<220>  
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 <222> (7)..(7)  
 <223> X = E OR G

<220>  
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 <222> (8)..(8)  
 <223> X = M OR K

<220>  
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 <222> (10)..(10)  
 <223> X = E OR D

<220>  
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 <222> (12)..(12)  
 <223> X = L OR I

<220>  
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 <222> (13)..(13)  
 <223> X = A OR T

<220>  
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 <222> (14)..(14)  
 <223> X = R, L, OR Q

<220>  
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 <222> (17)..(17)  
 <223> X = N OR D

<220>  
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 <222> (24)..(24)  
 <223> X = M OR E

<220>  
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 <222> (27)..(27)  
 <223> X = H OR L

<220>  
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 <222> (28)..(28)  
 <223> X = H OR Q

<220>  
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 <222> (29)..(29)  
 <223> X = Q, K OR M

<220>  
 <221> MISC\_FEATURE  
 <222> (30)..(30)  
 <223> X = N OR I

<220>  
 <221> MISC\_FEATURE  
 <222> (31)..(31)  
 <223> X = L OR Q

<220>  
 <221> MISC\_FEATURE  
 <222> (36)..(36)  
 <223> X = T OR A

<220>  
 <221> MISC\_FEATURE  
 <222> (38)..(38)  
 <223> X = K OR Q

<220>  
 <221> MISC\_FEATURE  
 <222> (40)..(40)  
 <223> X = V OR A

<220>  
 <221> MISC\_FEATURE  
 <222> (43)..(43)  
 <223> X = C, F OR S

<400> 40

Ser Xaa Xaa Glu Leu Lys Xaa Xaa Ile Xaa Thr Xaa Xaa Xaa Lys Leu  
 1 5 10 15

Xaa Glu Lys Ser Lys Glu Gln Xaa Glu Leu Xaa Xaa Xaa Xaa Xaa Asn  
 20 25 30

Leu Gln Glu Xaa Leu Xaa Arg Xaa Ala Asn Xaa Ser  
 35 40